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FIG. 1

TGGGCACAGC	CACCCTGTTG	GTAGTCCAGG	GGCCAGCCCA	CTGAGCTGGC	ATATCAGCTG	50
GTGGCCCCGT	TGGACTCGGC	CCTAGGGAAC	GGCGGCG	ATG GGA GCG CCC CGG ATC	115	
				Met Gly Ala Pro Arg Ile	1	5
TCG CAC AGC CTT GCC TTG CTC CTC TGC TGC TCC GTG CTC AGC TCC GTC	157					
Ser His Ser Leu Ala Leu Leu Leu Cys Cys Ser Val Leu Ser Ser Val						
	10			15		20
TAC GCA CTG GTG GAT GCC GAT GAT GTC ATA ACG AAG GAG GAG CAG ATC	211					
Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile						
	25			30		35
ATT CTT CTG CGC AAT GCC CAG GCC CAG TGT GAG CAG CGC CTG AAA GAG	259					
Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Leu Lys Glu						
	40			45		50
GTC CTC AGG GTC CCT GAA CTT GCT GAA TCT GCC AAA GAC TGG ATG TCA	307					
Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser						
	55			60		65
AGG TCT GCA AAG ACA AAG AAG GAG AAA CCT GCA GAA AAG CTT TAT CCC	355					
Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro						
	75			80		85
CAG GCA GAG GAG TCC AGG GAA GTT TCT GAC AGG AGC CGG CTG CAG GAT	403					
Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp						
	90			95		100
AGC TTC TGC CTA CTT GAG TGG AAC AAC ATT GTG TGC TGG CTT GCT GGA	411					
Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Ala Gly						
	105			110		115
GTG CCC GGC AAG GTG GTG GCC GTG CCC TGC CCC GAC TAC TTC TAC GAC	499					
Val Pro Gly Lys Val Val Ala Val Pro Cys Pro Asp Tyr Phe Tyr Asp						
	120			125		130
TTC AAC CAC AAA GGC CGA GCC TAT CGG CGC TGT GAC AGC AAT GGC AGC	547					
Phe Asn His Lys Gly Arg Ala Tyr Arg Arg Cys Asp Ser Asn Gly Ser						
	135			140		145
TGG GAG CTG GTG CCT GGG AAC AAC CGG ACA TGG GCG AAT TAC AGC GAA	595					
Trp Glu Leu Val Pro Gly Asn Asn Arg Thr Trp Ala Asn Tyr Ser Glu						
	155			160		165
TGT GTC AAG TTT CTG ACC AAC GAG ACC CGG GAA CGG GAA GTC TTT GAT	643					
Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp						
	170			175		180

GCTCTT = 74355T60

FIG. 1

CGC	CTC	GGA	ATG	ATC	TAC	ACT	GTG	GGC	TAC	TCC	ATC	TCT	CTG	GGC	TCC	691
Arg	Leu	Gly	Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Ile	Ser	Leu	Gly	Ser	
		185					190					195				
CTC	ACT	GTG	GCT	GTG	CTG	ATT	CTG	GGT	TAC	TTT	AGG	AGG	TTA	CAT	TGC	739
Leu	Thr	Val	Ala	Val	Leu	Ile	Leu	Gly	Tyr	Phe	Arg	Arg	Leu	His	Cys	
	200					205					210					
ACC	CGA	AAC	TAC	ATT	CAC	ATG	CAT	CTC	TTC	GTG	TCC	TTT	ATG	CTC	CGG	787
Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	
	215				220					225					230	
GCT	GTA	AGC	ATC	TTC	ATC	AAG	GAT	GCT	GTG	CTC	TAC	TCG	GGG	GTT	TCC	835
Ala	Val	Ser	Ile	Phe	Ile	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Val	Ser	
				235					240					245		
ACA	GAT	GAA	ATC	GAG	CGC	ATC	ACC	GAG	GAG	GAG	CTG	AGG	GCC	TTC	ACA	883
Thr	Asp	Glu	Ile	Glu	Arg	Ile	Thr	Glu	Glu	Glu	Leu	Arg	Ala	Phe	Thr	
			250					255					260			
GAG	CCT	CCC	CCT	GCT	GAC	AAG	GGC	GGT	TTT	GTG	GGC	TGC	AGA	GTG	GGC	931
Glu	Pro	Pro	Pro	Ala	Asp	Lys	Ala	Gly	Phe	Val	Gly	Cys	Arg	Val	Ala	
		265					270					275				
GTA	ACC	GTC	TTC	CTT	TAC	TTC	CTG	ACC	ACC	AAC	TAC	TAC	TGG	ATC	CTG	979
Val	Thr	Val	Phe	Leu	Tyr	Phe	Leu	Thr	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	
	280					285					290					
GTG	GAA	GGC	CTC	TAC	CTT	CAC	AGC	CTC	ATC	TTC	ATG	GCT	TTT	TTC	TCT	1027
Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	
	295				300					305					310	
GAG	AAA	AAG	TAT	CTC	TGG	GGT	CTC	ACA	TTA	TTT	GGC	TGG	GGC	CTC	CCT	1075
Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Leu	Phe	Gly	Trp	Gly	Leu	Pro	
				315					320					325		
ACC	ATG	TTT	CTC	GCT	GTG	TGG	CTC	ACC	ATG	AGG	GCT	ACA	CTG	GCC	AAC	1123
Ala	Val	Phe	Val	Ala	Val	Trp	Val	Thr	Val	Arg	Ala	Thr	Leu	Ala	Asn	
			330					335					340			
ACT	GAG	TGC	TGG	GAC	CTG	AGT	TCC	GGG	AAT	AAG	AAA	TGG	ATC	ATA	CAG	1171
Thr	Glu	Cys	Trp	Asp	Leu	Ser	Ser	Gly	Asn	Lys	Lys	Trp	Ile	Ile	Gln	
		345					350					355				
GTG	CCC	ATC	CTG	GCA	GCT	ATT	GTG	CTG	AAC	TTT	ATT	CTT	TTT	ATC	AAT	1219
Val	Pro	Ile	Leu	Ala	Ala	Ile	Val	Val	Asn	Phe	Ile	Leu	Phe	Ile	Asn	
	360					365					370					
ATA	ATC	AGA	GTC	CTG	GCT	ACT	AAA	CTC	GGG	GAG	ACC	AAT	GCA	GGG	AGA	1267
Ile	Ile	Arg	Val	Leu	Ala	Thr	Lys	Leu	Arg	Glu	Thr	Asn	Ala	Gly	Arg	
	375				380					385					390	

GAGTCTT = 42366T60



FIG. 2

TGGGCACAGC CACCCTGTTG GTAGTCCAGG GGCCAGCCCA CTGAGCTGGC ATATCAGCTG	60
GTGGCCCCGT TGGACTCGGC CCTAGGGAAC GGCGGCG ATG GGA GCG CCC CGG ATC	115
Met Gly Ala Pro Arg Ile	5
TCG CAC AGC CTT GCC TTG CTC CTC TGC TGC TCC GTG CTC AGC TCC GTC	163
Ser His Ser Leu Ala Leu Leu Cys Cys Ser Val Leu Ser Ser Val	10 15 20
TAC GCA CTG GTG GAT GCC GAT CAT GTC ATA ACG AAG GAG GAG CAG ATC	211
Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile	25 30 35
ATT CTT CTG CGC AAT GCC CAG GCC CAG TGT GAG CAG CGC CTG AAA GAG	259
Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Leu Lys Glu	40 45 50
GTC CTC AGG GTC CCT GAA CTT GCT GAA TCT GCC AAA GAC TGG ATG TCA	307
Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser	55 60 65 70
AGG TCT GCA AAG ACA AAG AAG GAG AAA CCT GCA GAA AAG CTT TAT CCC	355
Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro	75 80 85
CAG GCA GAG GAG TCC AGG GAA GTT TCT GAC AGG AGC CGG CTG CAG GAT	403
Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp	90 95 100
GGC TTC TGC CTA CCT GAG TGG GAC AAC ATT GTG TGC TGG CCT GCT GGA	451
Gly Phe Cys Leu Pro Glu Thr Ser Ile Val Cys Trp Pro Ala Gly	105 110 115
GTG CCC GGC AAG GTG GTG GCC CTC ACC TGC CCC GAC TAC TTC TAC GAC	499
Val Pro Gly Lys Val Val Ala Val Phe Cys Pro Asp Tyr Phe Tyr Asp	120 125 130
TTC AAC CAC AAA GGC CGA GCC TAT GGC CGC TGT GAC AGC AAT GGC AGC	547
Phe Asn His Lys Gly Arg Ala Tyr Arg Arg Cys Asp Ser Asn Gly Ser	135 140 145 150
TGG GAG CTG GTG CCT GGG AAC AAC GCG ACA TGG GCG AAT TAC AGC GAA	595
Trp Glu Leu Val Pro Gly Asn Asn Arg Thr Trp Ala Asn Tyr Ser Glu	155 160 165
TGT GTC AAG TTT CTG ACC AAC GAG ACC CGG GAA CGG GAA GTC TTT GAT	643
Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp	170 175 180

CGC CTC GGA ATG ATC TAC ACT GTG GGC TAC TCC ATC TCT CTG GGC TCC	691
Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Ile Ser Leu Gly Ser	
185 190 195	
CTC ACT GTG GCT GTG CTG ATT CTG GGT TAC TTT AGG AGG TTA CAT TGC	773
Leu Thr Val Ala Val Leu Ile Leu Gly Tyr Phe Arg Arg Leu His Cys	
200 205 210	
ACC CGA AAC TAC ATT CAC ATG CAT CTC TTC GTG TCC TTT ATG CTC CGG	737
Thr Arg Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg	
215 220 225 230	
GCT GTA AGC ATC TTC ATC AAG GAT GCT GTG CTC TAC TCG GGG GTT TCC	833
Ala Val Ser Ile Phe Ile Lys Asp Ala Val Leu Tyr Ser Gly Val Ser	
235 240 245	
ACA GAT GAA ATC GAG CGC ATC ACC GAG GAG GAG CTG AGG GCC TTC ACA	883
Thr Asp Glu Ile Glu Arg Ile Thr Glu Glu Glu Leu Arg Ala Phe Thr	
250 255 260	
GAG CCT CCC COT GCT GAC AAG GCG GGT TTT GTG GGC TGC AGA GTG GCG	931
Glu Pro Pro Pro Ala Asp Lys Ala Gly Phe Val Gly Cys Arg Val Ala	
265 270 275	
GTA ACC GTC TTC CTT TAC TTC CTG ACC ACC AAC TAC TAC TGG ATC CTG	973
Val Thr Val Phe Leu Tyr Phe Leu Thr Thr Asn Tyr Tyr Trp Ile Leu	
280 285 290	
GTG GAA GGC CTC TAC CTT CAC AGC CTC ATC TTC ATG GCT TTT TTC TCT	1027
Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser	
295 300 305 310	
GAG AAA AAG TAT CTC TGG GGT TTC ACA TTA TTT GGC TGG GGC CTC CCT	1073
Glu Lys Lys Tyr Leu Trp Gly Phe Thr Leu Phe Gly Trp Gly Leu Pro	
315 320 325	
GCC GTG TTT GTC GCT GTG TGG GTG ACC GTG AGG GCT ACA CTG GCC AAC	1123
Ala Val Phe Val Ala Val Trp Val Thr Val Arg Ala Thr Leu Ala Asn	
330 335 340	
ACT GAG TGC TGG GAC CTG AGT TCG GGG AAT AAG AAA TGG ATC ATA CAG	1171
Thr Glu Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln	
345 350 355	
GTG CCC ATC CTG GCA GCT ATT GTG GTG AAC TTT ATT CTT TTT ATC AAT	1219
Val Pro Ile Leu Ala Ala Ile Val Val Asn Phe Ile Leu Phe Ile Asn	
360 365 370	
ATA ATC AGA GTC CTG GCT ACT AAA CTC CGG GAG ACC AAT GCA GGG AGA	1267
Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg	
375 380 385 390	

TGT Cys	GAC Asp	ACG Thr	AGG Arg	CAA Gln 395	CAG Gln	TAT Tyr	AGA Arg	AAG Lys	CTG Leu 400	CTG Leu	AAG Lys	TCC Ser	ACG Thr	CTA Leu 405	GTC Val	1315
CTC Leu	ATG Met	CCG Pro	CTA Leu 410	TTT Phe	GGG Gly	GTG Val	CAC His	TAC Tyr 415	ATC Ile	GTC Val	TTC Phe	ATG Met	GCC Ala 420	ACG Thr	CCG Pro	1363
TAC Tyr	ACA Thr	GAA Glu 425	GTA Val	TCA Ser	GGG Gly	ATT Ile	CTT Leu 430	TGG Trp	CAA Gln	GTC Val	CAA Gln	ATG Met 435	CAC His	TAT Tyr	GAA Glu	1411
ATG Met 440	CTC Leu	TTC Phe	AAT Asn	TCA Ser	TTC Phe	CAG Gln 445	GGA Gly	TTT Phe	TTC Phe	GTT Val	GCC Ala 450	ATT Ile	ATA Ile	TAC Tyr	TGT Cys	1459
TTC Phe 455	TGC Cys	AAT Asn	GGA Gly	GAG Glu	GTA Val 460	CAA Gln	GCA Ala	GAG Glu	ATC Ile	AAG Lys 465	AAG Lys	TCA Ser	TGG Trp	AGC Ser	CGA Arg 470	1507
TGG Trp	ACC Thr	CTG Leu	GCC Ala	TTG Leu 475	GAC Asp	TTC Phe	AAG Lys	CGG Arg	AAG Lys 480	GCC Ala	CGG Arg	AGT Ser	GGC Gly	AGC Ser 485	AGT Ser	1555
ACC Thr	TAC Tyr	AGC Ser	TAT Tyr 490	GGC Gly	CCC Pro	ATG Met	GTG Val	TCA Ser 495	CAT His	ACA Thr	AGT Ser	GTC Val	ACC Thr 500	AAT Asn	GTG Val	1603
GGA Gly	CCT Pro	CGA Arg 505	GGG Gly	GGG Gly	CTG Leu	GCC Ala	TTG Leu 510	TCC Ser	CTC Leu	AGC Ser	CCT Pro	CGA Arg 515	CTA Leu	GCT Ala	CCT Pro	1651
GGG Gly 520	GCT Ala	GGA Gly	GCC Ala	AGT Ser	GCC Ala	AAT Asn 525	GGC Gly	CAT His	CAC His	CAG Gln	TTG Leu 530	CCT Pro	GGC Gly	TAT Tyr	GTG Val	1699
AAG Lys 535	CAT His	GGT Gly	TCC Ser	ATT Ile	TCT Ser	GAG Glu 540	AAC Asn	ACA Ser	TTG Leu	CCT Pro 545	TCA Ser	TCT Ser	GGC Gly	CCA Pro	GAG Glu 550	1747
CCT Pro	GGC Gly	ACC Thr	AAA Lys	GAT Asp 555	GAC Asp	GGG Gly	TAT Tyr	CTC Leu	AAT Asn 560	GGC Gly	TCT Ser	GGA Gly	CTT Leu 565	TAT Tyr	GAG Glu	1795
CCA Pro	ATG Met	GTT Val	GGG Gly 570	GAA Glu	CAG Gln	CCC Pro	CCT Pro	CCA Pro 575	CTC Leu	CTG Leu	GAG Glu	GAG Glu	GAG Glu 580	AGA Arg	GAG Glu	1843
ACA Thr	GTC Val	ATG Met 585	TGACCCATAT C													1863

CGTCTT=43866T60

GGCGGGGGCC	GCGGCGGCGA	GCTCGGAGGC	CGGCGGCGGC	TGCCCCGAGG	GACGCGGCCC	60										
TAGGCGGTGG	CG	ATG	GGG	GCC	GCC	CGG	ATC	GCA	CCC	AGC	CTG	GCG	CTC	108		
	1						5					10				
CTA	CTC	TGC	TGC	CCA	GTG	CTC	AGC	TCC	GCA	TAT	GCG	CTG	GTG	GAT	GCG	120
Leu	Leu	Cys	Cys	Pro	Val	Leu	Ser	Ser	Ala	Tyr	Ala	Leu	Val	Asp	Ala	
		15					20					25				
GAC	GAT	GTC	TTT	ACC	AAA	GAG	GAA	CAG	ATT	TTC	CTG	CTG	CAC	CGT	GCC	204
Asp	Asp	Val	Phe	Thr	Lys	Glu	Glu	Gln	Ile	Phe	Leu	Leu	His	Arg	Ala	
	30					35					40					
CAG	GCG	CAA	TGT	GAC	AAG	CTG	CTC	AAG	GAA	GTT	CTG	CAC	ACA	GCA	GCC	228
Gln	Ala	Gln	Cys	Asp	Lys	Leu	Leu	Lys	Glu	Val	Leu	His	Thr	Ala	Ala	
	45				50				55						60	
AAC	ATA	ATG	GAG	TCA	GAC	AAG	GGC	TGG	ACA	CCA	GCA	TCT	ACG	TCA	GGG	300
Asn	Ile	Met	Glu	Ser	Asp	Lys	Gly	Trp	Thr	Pro	Ala	Ser	Thr	Ser	Gly	
				65				70						75		
AAG	CCC	AGG	AAA	GAG	AAG	GCA	TCG	GGA	AAG	TTC	TAC	CCT	GAG	TCT	AAA	348
Lys	Pro	Arg	Lys	Glu	Lys	Ala	Ser	Gly	Lys	Phe	Tyr	Pro	Glu	Ser	Lys	
			80					85					90			
GAG	AAC	AAG	GAC	GTG	CCC	ACC	GGC	AGC	AGG	CGC	AGA	GGG	CGT	CCC	TGT	396
Glu	Asn	Lys	Asp	Val	Pro	Thr	Gly	Ser	Arg	Arg	Arg	Gly	Arg	Pro	Cys	
		95					100					105				
CTG	CCC	GAG	TGG	GAC	AAC	ATC	GTT	TGC	TGG	CCA	TTA	GGG	GCA	CCA	GGT	444
Leu	Pro	Glu	Trp	Asp	Asn	Ile	Val	Cys	Trp	Pro	Leu	Gly	Ala	Pro	Gly	
	110					115					120					
GAA	GTG	GTG	GCA	GTA	CCT	TGT	CCC	GAT	TAC	ATT	TAT	GAC	TTC	AAT	CAC	492
Glu	Val	Val	Ala	Val	Pro	Cys	Pro	Asp	Tyr	Ile	Tyr	Asp	Phe	Asn	His	
	125				130					135					140	
AAA	GGC	CAT	GCC	TAC	AGA	CGC	TGT	GAC	CGC	AAT	GGC	AGC	TGG	GAG	GTG	540
Lys	Gly	His	Ala	Tyr	Arg	Arg	Cys	Asp	Arg	Asn	Gly	Ser	Trp	Glu	Val	
				145				150					155			
GTT	CCA	GGG	CAC	AAC	CGG	ACG	TGG	GCC	AAC	TAC	AGC	GAG	TGC	CTC	AAG	588
Val	Pro	Gly	His	Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu	Cys	Leu	Lys	
			160					165					170			
TTC	ATG	ACC	AAT	GAG	ACG	CGG	GAA	CGG	GAG	GTA	TTT	GAC	CGC	CTA	GGC	636
Phe	Met	Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	Arg	Leu	Gly	
		175					180					185				
ATG	ATC	TAC	ACC	GTG	GGA	TAC	TCC	ATG	TCT	CTC	GCC	TCC	CTC	ACG	GTG	684
Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Met	Ser	Leu	Ala	Ser	Leu	Thr	Val	
	190					195					200					

GGTCTT-1206T60



GCT Ala 205	GTG Val	CTC Leu	ATC Ile	CTG Leu	GCC Ala 210	TAT Tyr	TTT Phe	AGG Arg	CGG Arg	CTG Leu 215	CAC His	TGC Cys	ACG Thr	CGC Arg	AAC Asn 220	732
TAC Tyr	ATC Ile	CAC His	ATG Met	CAC His 225	ATG Met	TTC Phe	CTG Leu	TCG Ser	TTT Phe 230	ATG Met	CTG Leu	CGC Arg	GCC Ala	CGC Ala 235	AGC Ser	780
ATC Ile	TTC Phe	GTG Val	AAG Lys 240	GAC Asp	GCT Ala	GTG Val	CTC Leu	TAC Tyr 245	TCT Ser	GGC Gly	TTC Phe	ACG Thr	CTG Leu 250	GAT Asp	GAG Glu	828
GCC Ala	GAG Glu	CGC Arg 255	CTC Leu	ACA Thr	GAG Glu	GAA Glu	GAG Glu 260	TTG Leu	CAC His	ATC Ile	ATC Ile	GCG Ala 265	CAG Gln	GTG Val	CCA Pro	876
CCT Pro 270	CCG Pro	CCG Pro	GCC Ala	GCT Ala	GCC Ala 275	GCC Ala	GTA Val	GGC Gly	TAC Tyr	GCT Ala	GGC Gly 280	TGC Cys	CGC Arg	GTG Val	GCG Ala	924
GTG Val 285	ACC Thr	TTC Phe	TTC Phe	CTC Leu 290	TAC Tyr	TTC Phe	CTG Leu	GCT Ala 295	ACC Thr	AAC Asn	TAC Tyr	TAC Tyr	TGG Trp	ATT Ile 300	CTG Leu	972
GTG Val	GAG Glu	GGG Gly	CTG Leu 305	TAC Tyr	TTG Leu	CAC His	AGC Ser	CTC Leu 310	ATC Ile	TTC Phe	ATG Met	GCC Ala	TTT Phe 315	TTC Phe	TCA Ser	1020
GAG Glu	AAG Lys	AAG Lys 320	TAC Tyr	CTG Leu	TGG Trp	GGC Gly	TTC Phe 325	ACC Thr	ATC Ile	TTT Phe	GGC Gly	TGG Trp 330	GGT Gly	CTA Leu	CCG Pro	1068
GCT Ala 335	GTG Val	TTC Phe	GTG Val	GCT Ala	GTG Val	TGG Trp 340	GTG Val	GCT Ala	GTG Val	AGA Arg	GCA Ala 345	ACC Thr	TTG Leu	GCC Ala	AAC Asn	1116
ACT Thr 350	GGG Gly	TGC Cys	TGG Trp	GAT Asp	CTG Leu 355	AGC Ser	TCC Ser	TGG Ala	CAC His	AAG Lys 360	AAG Lys	TGG Trp	ATC Ile	ATC Ile	CAG Gln 365	1164
GTG Val	CCC Pro	ATC Ile	CTG Leu	GCA Ala 370	TCT Ser	GTT Val	GTG Val	CTC Leu 375	AAC Asn	TTC Phe	ATC Ile	CTT Leu	TTT Phe 380	ATC Ile	AAC Asn	1212
ATC Ile	ATC Ile	CGG Arg	GTG Val 385	CTT Leu	GCC Ala	ACT Thr	AAG Lys	CTT Leu 390	CGG Arg	GAG Glu	ACC Thr	AAT Asn	GCG Ala 395	GGC Gly	CGG Arg	1260
TGT Cys	GAC Asp	ACC Thr 400	AGG Arg	CAG Gln	CAG Gln	TAC Tyr	CGG Arg 405	AAG Lys	CTG Leu	CTC Leu	AGG Arg	TCC Ser	ACG Thr 410	TTG Leu	GTG Val	1308

CTC	GTG	CCG	CTC	TTT	GGT	GTC	CAC	TAC	ACC	GTC	TTC	ATG	GCC	TTG	CCG	1356
Leu	Val	Pro	Leu	Phe	Gly	Val	His	Tyr	Thr	Val	Phe	Met	Ala	Leu	Pro	
415						420					425					
TAC	ACC	GAG	GTC	TCA	GGG	ACA	TTG	TGG	CAG	ATC	CAG	ATG	CAT	TAT	GAG	1404
Tyr	Thr	Glu	Val	Ser	Gly	Thr	Leu	Trp	Gln	Ile	Gln	Met	His	Tyr	Glu	
430					435					440					445	
ATG	CTC	TTC	AAC	TCC	TTC	CAG	GGA	TTT	TTT	GTT	GCC	ATC	ATA	TAC	TGT	1452
Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	
				450					455					460		
TTC	TGC	AAT	GGT	GAG	GTG	CAG	GCA	GAG	ATT	AGG	AAG	TCA	TGG	AGC	CGC	1500
Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Arg	Lys	Ser	Trp	Ser	Arg	
			465					470					475			
TGG	ACA	CTG	GCG	TTG	GAC	TTC	AAG	CGC	AAA	GCA	CSA	AGT	GGG	AGT	AGC	1548
Trp	Thr	Leu	Ala	Leu	Asp	Phe	Lys	Arg	Lys	Ala	Arg	Ser	Gly	Ser	Ser	
			480				485					490				
AGC	TAC	AGC	TAT	GGC	CCA	ATG	GTG	TCT	CAC	ACG	AGT	GTG	ACC	AAT	GTG	1596
Ser	Tyr	Ser	Tyr	Gly	Pro	Met	Val	Ser	His	Thr	Ser	Val	Thr	Asn	Val	
	495					500					505					
GGC	CCC	CGT	GCA	GGA	CTC	AGC	CTC	CCC	CTC	AGC	CCC	CGC	CTG	CCT	CCT	1644
Gly	Pro	Arg	Ala	Gly	Leu	Ser	Leu	Pro	Leu	Ser	Pro	Arg	Leu	Pro	Pro	
510					515					520					525	
GCC	ACT	ACC	AAT	GGC	CAC	TCC	CAG	CTG	CCT	GGC	CAT	GCC	AAG	CCA	GGG	1692
Ala	Thr	Thr	Asn	Gly	His	Ser	Gln	Leu	Pro	Gly	His	Ala	Lys	Pro	Gly	
				530					535					540		
GCT	CCA	GCC	ACT	GAG	ACT	GAA	ACC	CTA	CCA	GTC	ACT	ATG	GCG	GTT	CCC	1740
Ala	Pro	Ala	Thr	Glu	Thr	Glu	Thr	Leu	Pro	Val	Thr	Met	Ala	Val	Pro	
			545					550					555			
AAG	GAC	GAT	GGA	ATC	CTT	AAC	GGC	TCC	TCC	TCA	GGC	CTG	GAT	GAG	GAG	1788
Lys	Asp	Asp	Gly	Phe	Leu	Asn	Gly	Ser	Cys	Ser	Gly	Leu	Asp	Glu	Glu	
		560					565					570				
GCC	TCC	GGG	TCT	GCG	CGG	CCG	CCT	CCA	TTG	TTG	CAG	GAA	GGA	TGG	GAA	1836
Ala	Ser	Gly	Ser	Ala	Arg	Pro	Pro	Pro	Leu	Leu	Gln	Glu	Gly	Trp	Glu	
	575					580					585					
ACA	GTC	ATG	TGACTGGGCA	CTAGGGGGCT	AGACTGCTGG	CCTGGGCACA	1885									
Thr	Val	Met					590									
TGGACAGATG	GACCAAGAAG	CCAGTGTTC	GCTSGTTGTC	TATTCGGGAT	CTGGACCAGG	1945										
AAGATAACAA	AAGGAAAATG	GAAGTGGACC	AAGCAGAGAA	GAAGGAAGAG	GTTTTGCAGG	2005										
AATTAAATAT	GTTTCCTCAG	TTGGATGATG	AGGACACAAG	GAAGGC		2051										

GCTCTT-72306760

1 MGAARIAPSLALLCCPVLSAYALVDADDVPTREEQIFLLHRAQAQCDX 50  
 1 NGAPRISHSLALLCCSVLSSVYALVDADDVITREEQIILLRNAQAQCEQ 50  
 51 LLKEVLHTAANIHESDKGWTTPASTSGKPRKERASGKFPYPSKEHKDVPTG 100  
 51 RLKEVLR.VPELAESAQDW..MSRSATKKEKPAEKLYPQAEZSREVSDR 97  
 101 SRRRGRPCLPENDNIVCWPPLGAPGEVVAVPCPDYIYDFNHRKGZAYRRCDB 150  
 98 SRLQDGFCLPENDNIVCWPAGVPGKVVAVPCPDYFYDFNHRKGZAYRRCDS 147  
 151 NGSWEVVPCHNRTWANYSECLAFMTNETREREVFDRLGMIYTYGYSMSLA 200  
 148 NGSWEVVPCHNRTWANYSECVKPLTNETREREVFDRLGMIYTYGYSISLG 197  
 201 SLTVAVLI:LAYFRRHCTRNHYIEMHMFLLSFLRAASIFVKDAVLYSGFTL 250  
 198 SLTVAVLI:LGTFRRHCTRNHYIEMHMLFVSFMLRAVSIFIKDAVLYSGVST 247  
 251 DEARLTEEELHIIAQVPPPPAAAAGVYAGCRVAVTFFLYFLATNYYWIL 300  
 148 DEIERITEELRAFTE...PPPADKAGFVGCRAVTVFLYFLTTNYYWIL 294  
 301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGNGLPVAVFVAVWVGVRATLANTG 350  
 195 VEGLYLHSLIFMAFFSEKKYLWGFTIFGNGLPVAVFVAVWVTVRATLANTE 344  
 351 CNDLSSGNKKRWIIOVPILASVVLNFIILFINI:RVLATKLRETNAGRCDB 400  
 345 CNDLSSGNKKRWIIOVPILAAIVVNFIILFINI:RVLATKLRETNAGRCDB 394  
 401 QOYRKLLRSTLVLPFLGVHYTVFMALPYTEVSGTLWQIQHMYEHLFNSF 450  
 195 QOYRKLLRSTLVLPFLGVHYIVFMATPYTETVSGTLWQVQHMYEHLFNSF 444  
 451 QGFFVAIIYCFNGEVOAEIRKSWSRWTLALDFKKKARSGSSSYSGPHV 500  
 445 QGFFVAIIYCFNGEVOAEIRKSWSRWTLALDFKKKARSGSSSYSGPHV 494  
 501 EHTSVTNVGFPRAGLSPLSPRLPP...ATTNCHSOLPGHAKPGAPATETE 547  
 495 EHTSVTNVGFPRAGLSPLSPRLAPGAGASANGHOLPGYVKHGSISENSL 544  
 548 TLVVTMAVPRKDDGFLNGSCSGLDEEASGSAFPPLQEGWETVR. 591  
 545 PSSGFEPGTRKDDGYLNG...SGLYEPMVG.EQFPPLLEZERETVR. 596

Gap Weight: 3.000      Average Match: 0.540  
 Length Weight: 0.100      Average Mismatch: -0.396  
 Quality: 712.2      Length: 595  
 Ratio: 1.215      Gaps: 6  
 Percent Similarity: 87.113      Percent Identity: 77.335

Sequence: 74360160

Fig. 5

```

R15 MGAARIAPSL ALLLCCPVLS SAYALVDADD VFTKEEQIFL LHRQAQCDK 50
Okh MGAPRISHSL ALLLCCSVLS SVYALVDADD VITKEEQIIL LRNAQAQCEQ 50
Okh MGAPRISHSL ALLLCCSVLS SVYALVDADD VITKEEQIIL LRNAQAQCEQ 50
----- A -----

R15 LLKEVLHTAA NIMESDKGWT PASTSGKPRK ERASGRFYFE SKENKDVPTG 100
Okh RLKEVLR.VP ELAESAKDW. .MSRSAKTKK EKPAEKLYPQ AEZSREVSQR 97
Okh RLKEVLR.VP ELAESAKDW. .MSRSAKTKK EKPAEKLYPQ AEZSREVSQR 97

R15 SRRRGRPCLP EWDNIVCWPL GAPGEVVAVP CPDYIYDFNH KGHAYRRCDR 150
Okh SRLQDGFCLP EWDNIVCWPA GVPGRVVAVP CPDYFYDFNH KGRAYRRCDR 147
Okh SRLQDGFCLP EWDNIVCWPA GVPGRVVAVP CPDYFYDFNH KGRAYRRCDR 147
----- B -----

R15 N N N N
Okh NGSWEVVP GH NRTWANYSEC LKFMNTNETRE REVFDRLGHI YTVGYSM SLA 200
Okh NGSWEVVP GH NRTWANYSEC VKFLTNETRE REVFDRLGHI YTVGYSSISLG 197
Okh NGSWEVVP GH NRTWANYSEC VKFLTNETRE REVFDRLGHI YTVGYSSISLG 197
----- C -----

R15 SLTVAVLILA YFRRLHCTRN YIHHMFLSF MLRAASIFVK DAVLYSGFTL 250
Okh SLTVAVLILG YFRRLHCTRN YIHHMFLVSP MLRAVSIFIK DAVLYSGVST 247
Okh SLTVAVLILG YFRRLHCTRN YIHHMFLVSP MLRAVSIFIK DAVLYSGVST 247
----- D -----

R15 DEAEERLTSEE LHIIAQVPPP PAAAVGYAG CRVAVTFPLY FLATNYYWIL 300
Okh DEIERITEEE LRAFTE...P PPADKAGFVG CRVAVTVPLY FLTTNYYWIL 294
Okh DEIERITEEE LRAFTE...P PPADKAGFVG CRVAVTVPLY FLTTNYYWIL 294
----- E -----

R15 VEGLYLHSLI FMAFFSEKKY LWGFTIFGWG LPAVFVAVWV GVRATLANTG 350
Okh VEGLYLHSLI FMAFFSEKKY LWGFTIFGWG LPAVFVAVWV TVRATLANTE 344
Okh VEGLYLHSLI FMAFFSEKKY LWGFTIFGWG LPAVFVAVWV TVRATLANTE 344
----- F -----

R15 CWDLSSGHRK WIIQVPILAS VVLNPFILFIN IIRVLATKLR ETNAGRCDDR 400
Okh CWDLSSGNKK WIIQVPILAA IVVNPFILFIN IIRVLATKLR ETNAGRCDDR 394
Okh CWDLSSGNKK WIIQVPILAA IVVNPFILFIN IIRVLATKLR ETNAGRCDDR 394
----- G -----

R15 QQYRKLLRST LVLVPLFGVH YTVFMALPYT EVSGTLWQIQ MHEMLFNST 450
Okh QQYRKLLKST LVLMPFLGVH YIVFMATPYT EVSGILWQVQ MHEMLFNST 444
Okh QQYRKLLKST LVLMPFLGVH YIVFMATPYT EVSGILWQVQ MHEMLFNST 444
----- H -----

R15 QGFFVAVIYC FCNGEVOAEI RKSWSRWTLA LDFKRRKARSG SSSYSYGPHV 500
Okh QGFFVAVIYC FCNGEVOAEI RKSWSRWTLA LDFKRRKARSG SSTYSYGPHV 494
Okh QGFFVAVIYC FCNGEVOAEI RKSWSRWTLA LDFKRRKARSG SSTYSYGPHV 494
----- I -----

R15 SHTSVTNVGP RAGLSLPLSP RLFP...ATT NGHSQLPGHA KPGAPATETE 547
Okh SHTSVTNVGP RGGLALSLSL RLAPGAGASA NGHHQLPGYV KHGSISENSL 544
Okh SHTSVTNVGP RGG..... .NCPGSA LD 515

R15 TLPVTMAVPR DDGFLNGSCS GLDEEASGSA RPPPLLQEGW ETVM 591
Okh PSSGPEPGTK DDGYLNG..S GLYEPHVG.E QPPPLLZEER ETVM 585

```

With 1 enzyme: SACT

M G T A R - A P G L A -

2  
GGGATCCCGCGGGCCCTAGGCGGGTGGCGGatgggGAccGCCcggatcgacccgggctggcg  
CCCTAGGGCGCGGGGATCCGCCACCGCtaccctTggCGggcctagcgtgggcccggaccgc  
M G T A R I A F G L A -  
62  
ctccctgctctgctgccccgtgctcagctccgctacgcgctggaggatgcagatgacgtc  
gaggacgagacgacggggcacgagtcgaggcgcatgcgcgaccacctacgtctactgcag  
L L L C C P V L S S A Y A L V D A D D V -  
122  
atgactaaagaggaacagatcttccctgctgccccgtgctcaggcccagtgcgaaaaacgg  
tactgtttttctctctgtctagaaggacgacgtggcagcagtcggggtcacgctttctgccc  
M T K E E Q I F L L H R A Q A Q C E K R -  
182  
ctcaaggaggctccctgcagaggccagccagcctaatggaatcagacaagggatggacatct  
gagttccctccaggacgtctccgggtcggtcgtattaccttagtctgttccctacctgtaga  
L K E V L Q R P A S I M E S D K G W T S -  
242  
gggtccacatcaggggaagcccggaagataaggcatctgggaagctctaccctgagttct  
ggcagggtgtagtccctctggggtcccttccattccctagacccttcgagatgggactcaga  
A S T S G K P R K D H A S G K L Y P E S -  
302  
gaggagggacaagggaggccaccactggcagcaggtaccgagggcgccctgtctgcccggaa  
ctccctccctgtccctccctggggtgaccgtctctccctccctccctggggggacagacggcctt  
E E C H E A P T E S I L R G R P C L P E -  
362  
ggggaccacatccctgtgctggccgctggggggccaccgctcaggtggtggctgtgcccgtg  
accctgggtgtaggacacgaccggcgaccccccgtgtccactccaccaccgacacggggaca  
W D H I L C W P L G A P S E V V A V P C -  
422  
ccggactacatcttatgacttcaatcacaaagggccatgcccaccgacgtgtgaccgcaat  
ggcctgagtgtaaatactgaagttagtggttccgggtacggatggctgcgacactggcgctta  
P D Y I Y D F N H K G A A Y R R C D R N -  
482  
ggcagctgggaagctgggtgctggggcacaacaggacccctggggccaactacagcgagtggtgc  
ccgtcgaccctcgaccacggaccctgttctccctgcacccgggttgatgtcgctcacacag  
541



1080 ----- 1141  
 acccttgaactcgaagccctctgtttttcacctagtaggtccacgggttaggacccggaggttaa  
 W D L S S G N K K W I I Q V P I L A S I -  
 1142 ----- 1201  
 caccgagttgaagtaggagaaagttagttatagcaggccacgagcgggtgggttcgtcgccctc  
 V L N F I L F I N I V R V L A T K Q R E -  
 1202 ----- 1261  
 accaacgcggcgccggtgtgacacacggcagcagtagccggaagctgctcaaattccacgctg  
 tgggttggggccggccacactgtgtgcggtcgttatggcccttcgacgagtttaggtgcgac  
 T N A G R C D T R I I V R K L L K S T L -  
 1262 ----- 1321  
 caccgagtagcggggagaaaccgcaggtgatgttaccagaagtaccgggtgtgggtatgtgggtc  
 V L M P L F G V H Y I V F M A T P Y T E -  
 1322 ----- 1381  
 cagagttccctgcgagaccgttcagggtctacgtctatactctacgagaagttgagggaaggctc  
 V S G T L W Q V Q M H Y E M L F N S F Q -  
 1382 ----- 1441  
 cctaaaaaacacgcgttagttatatgacaaaagacgttaccggtccatgttcgactctagttc  
 G F F V A I I Y C F C N S E V Q A E I K -  
 1442 ----- 1501  
 tttagaacctcggggacgtgtgacctgtaccttaacttcggttcggttcgcccccg  
 K S W S R W T L A L I F H R K A R S G S -  
 1502 ----- 1561  
 tccctcgtatccgatccgggggtaccacacgggtttgtccacactgggttacagccgggggca  
 S S Y S Y G F M V S H T S V T N V G P R -  
 1562 ----- 1621  
 caccctgagcccgacggggagtccggggggcggtatccgggtgacgggtgggtgggttgcgggtg  
 V G L G L P L S P R L L F T A T T N G H -  
 1622 ----- 1681  
 ggaagtcgacgggacccgtacgggttcgggtccctgggttcgggacctctgggagctctgggtgt  
 F Q L P G H A K P G T F A L E T L E T T -





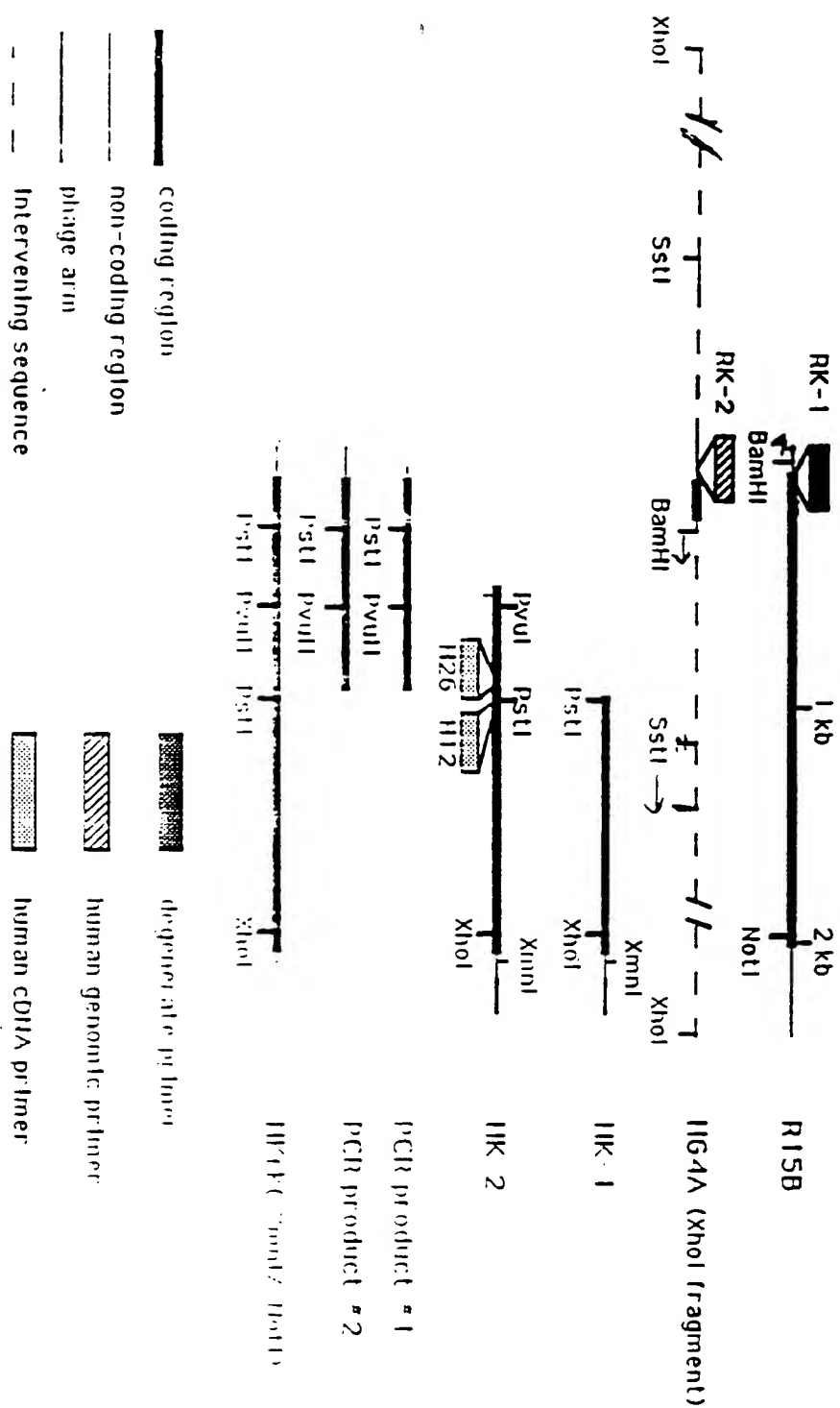


Fig. 7

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 TRAFFIC of: HK.seq ck: 9754 from: 29 to: 1810

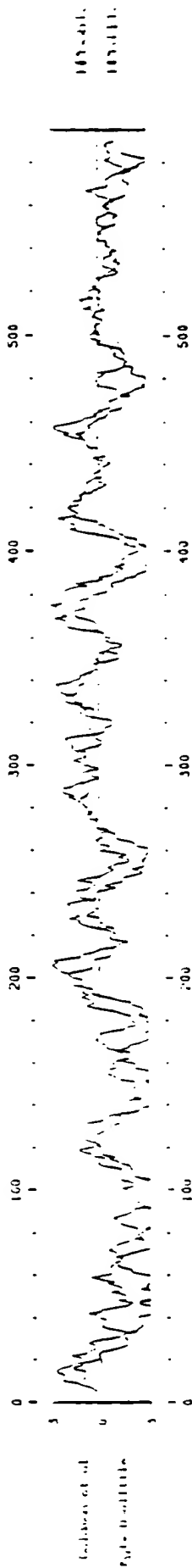


FIG. 9

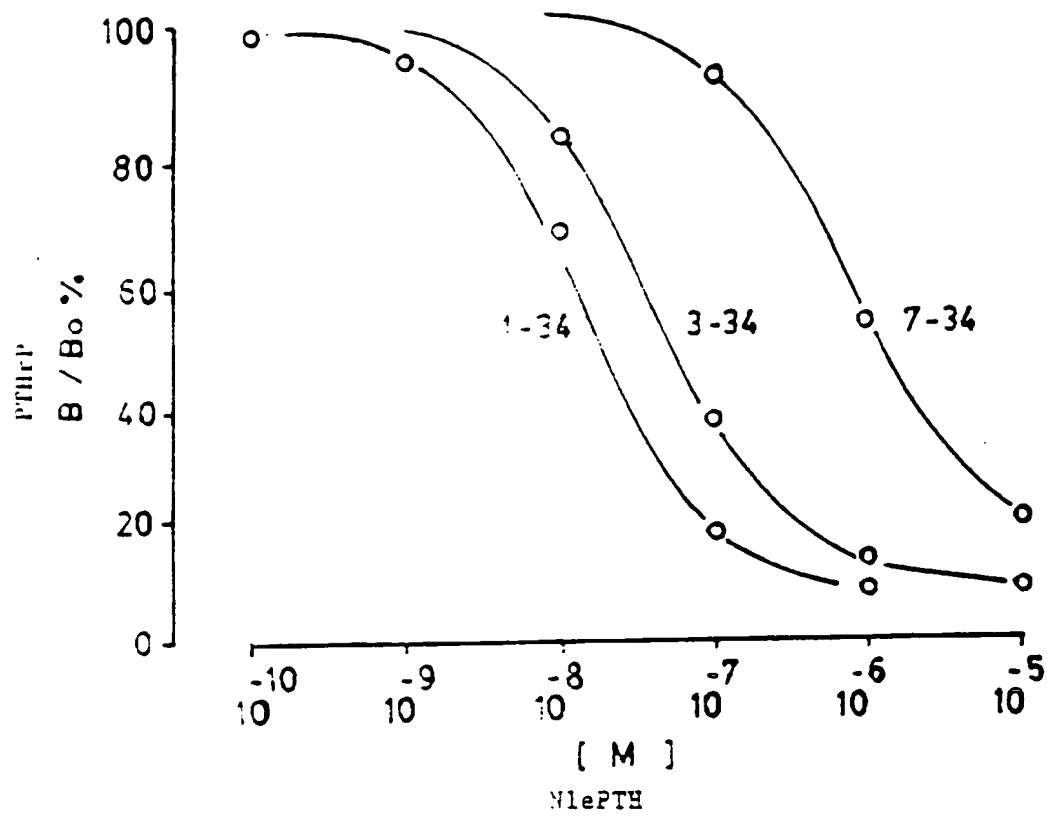


FIG. 10

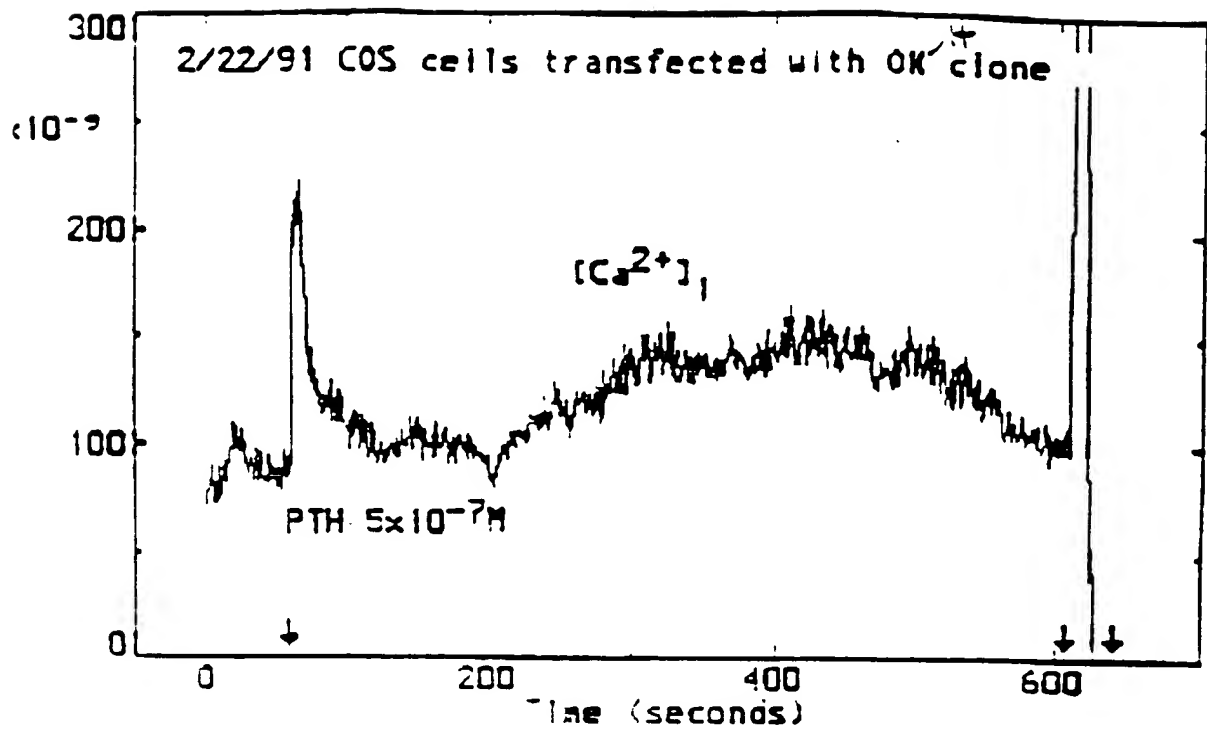


Fig. 11

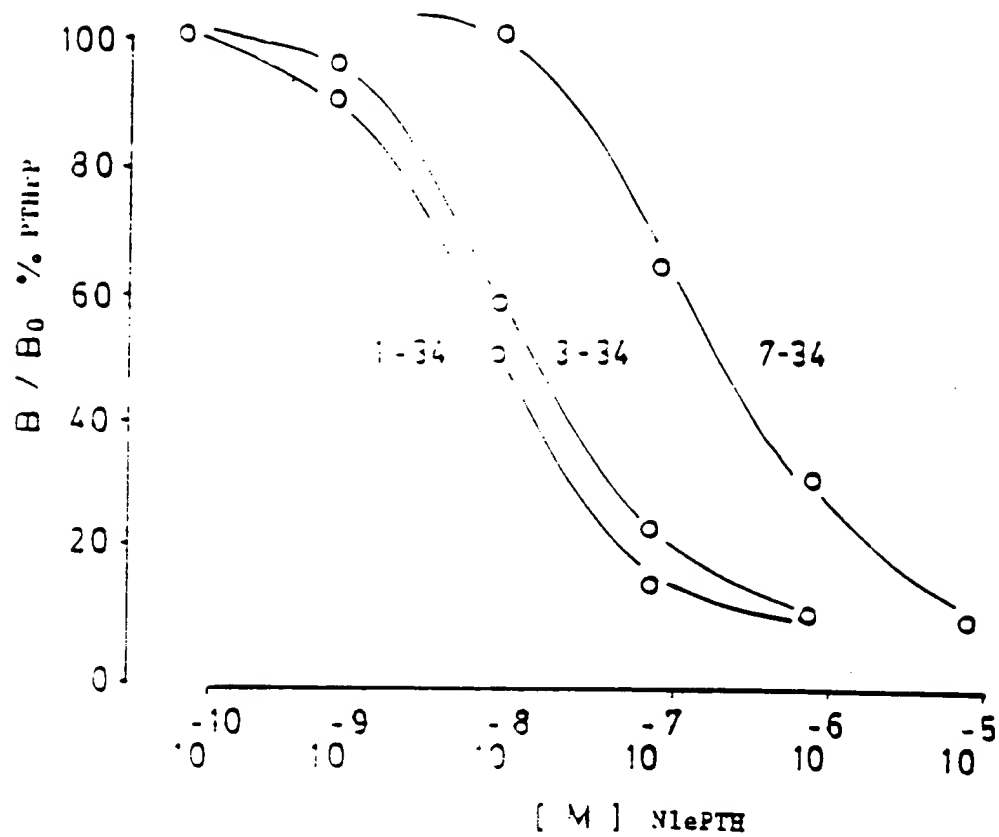
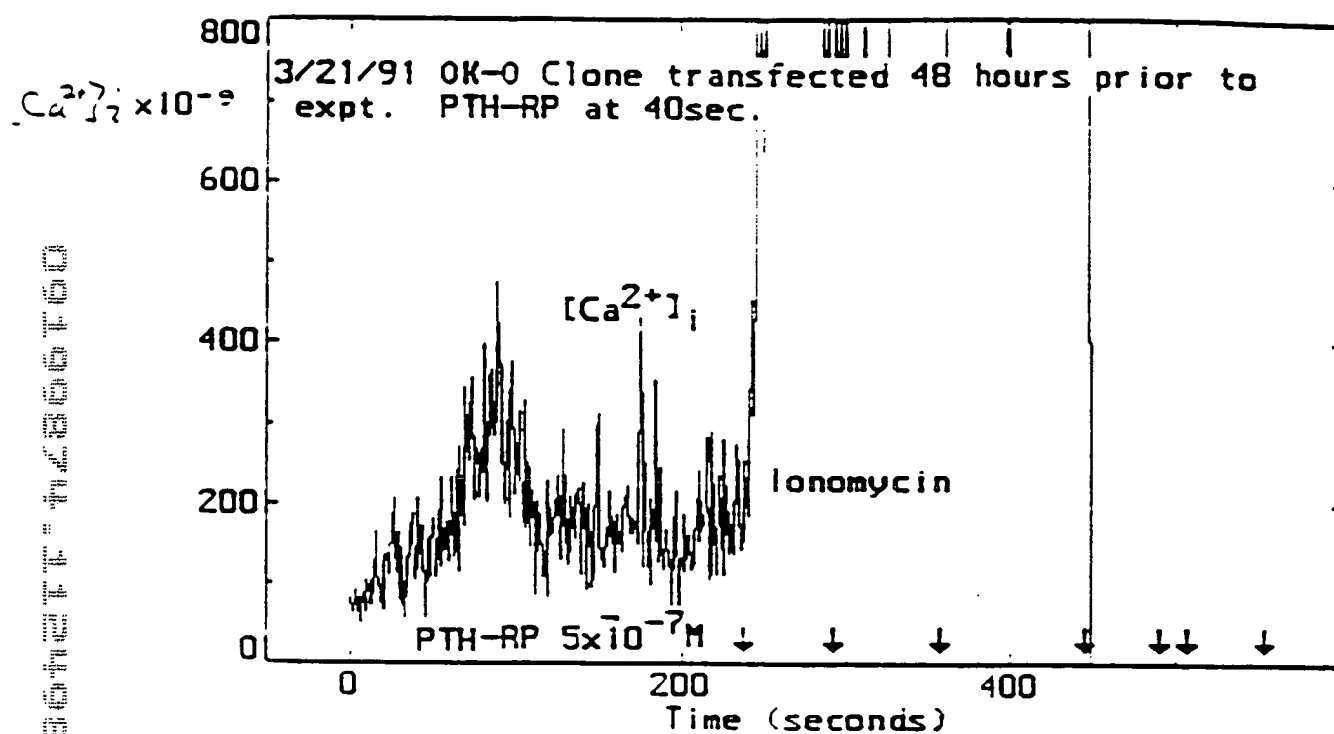


FIG.12



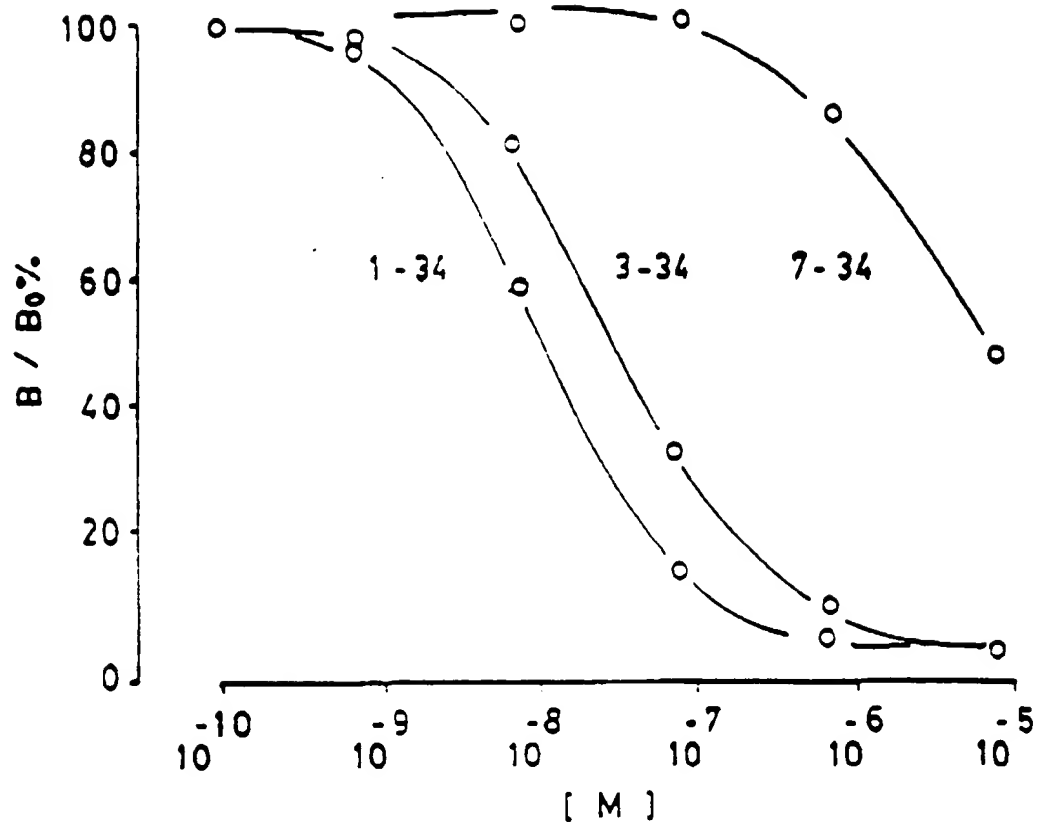


FIG. 13

FIG. 14

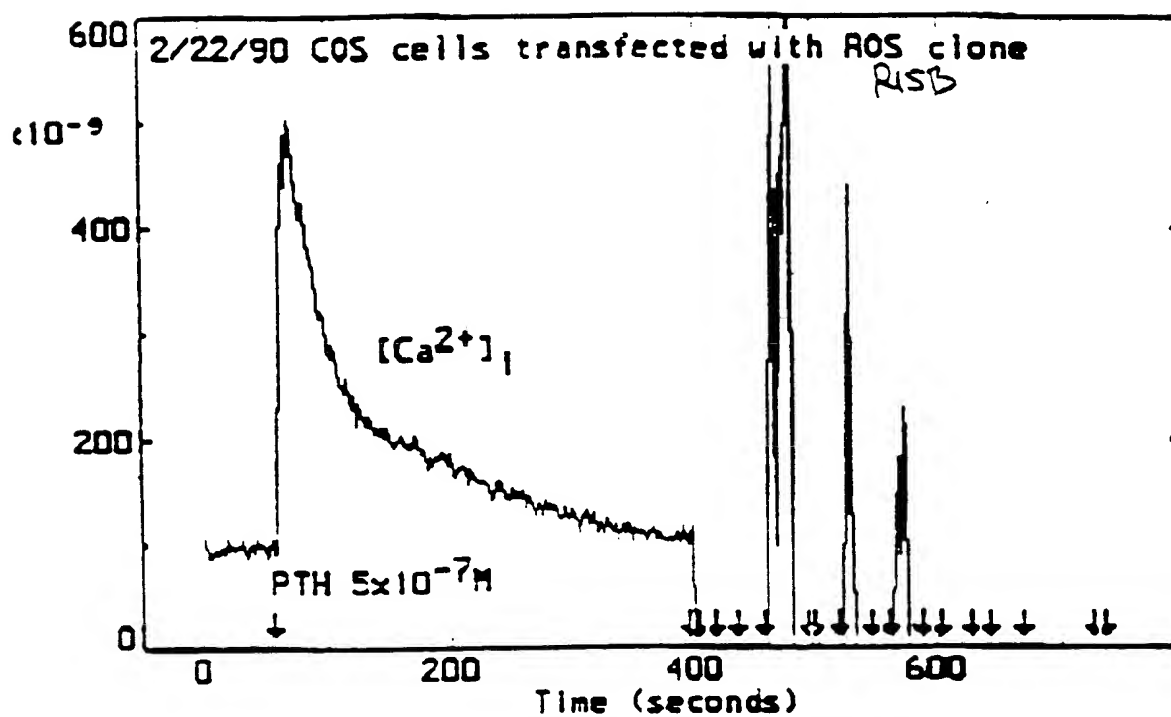




FIG. 15

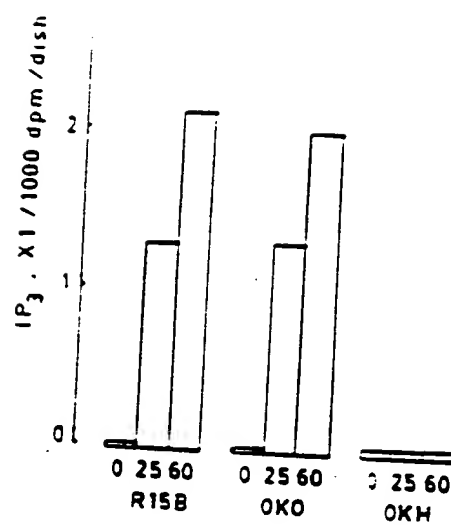
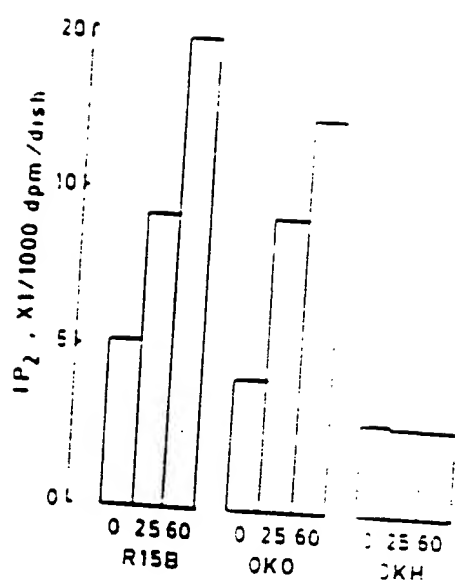
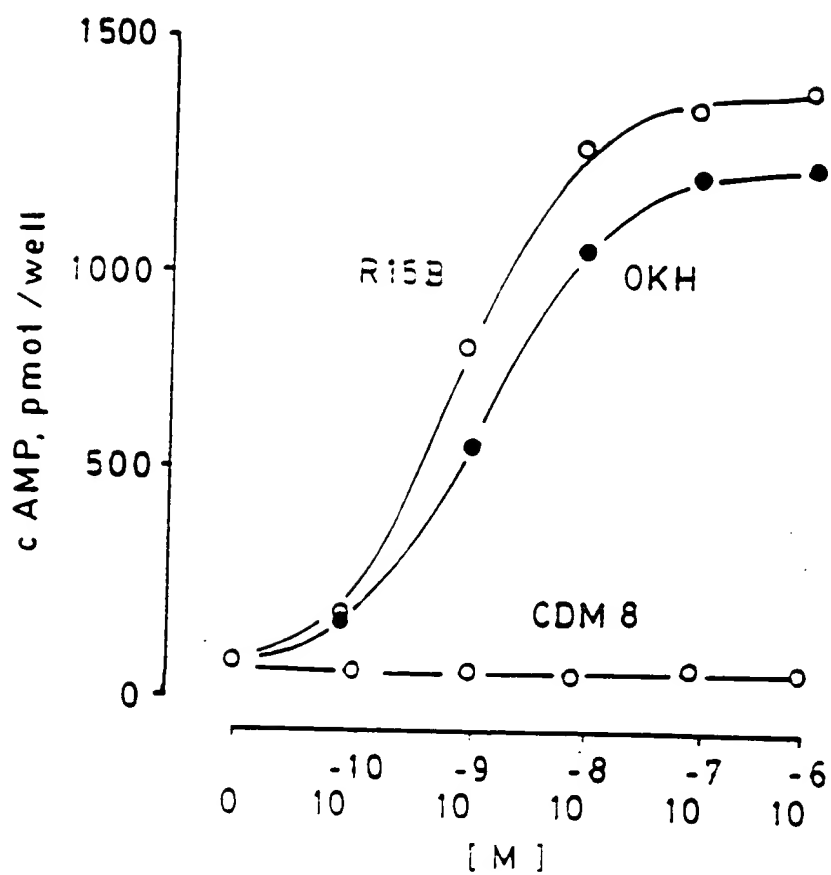
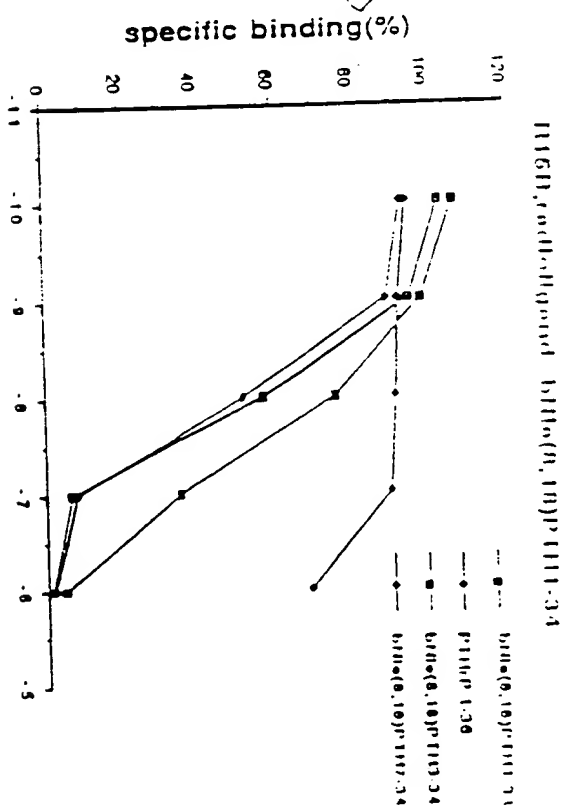
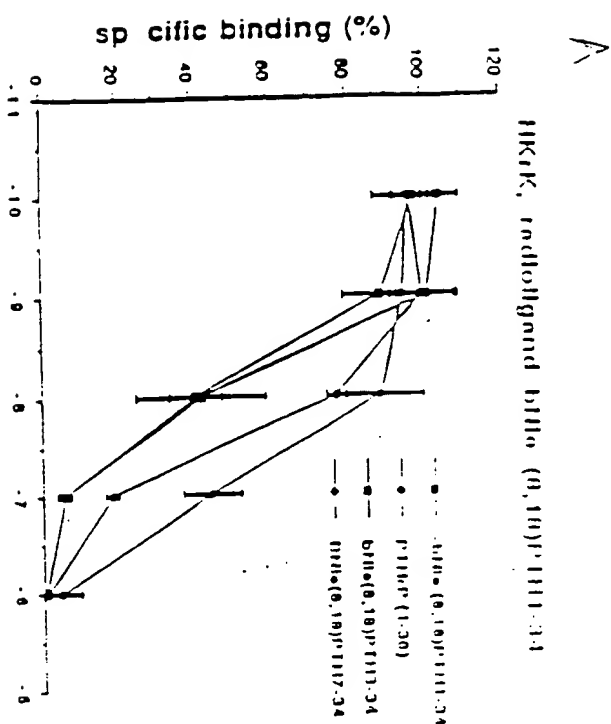
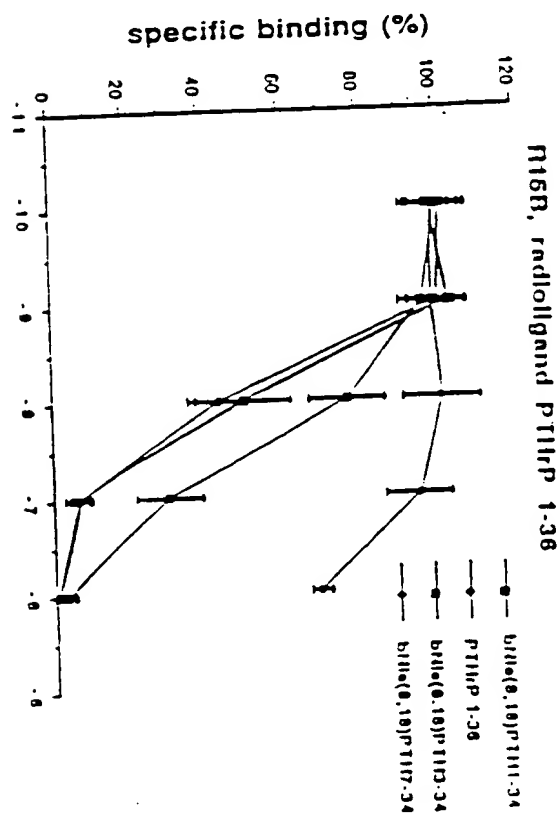
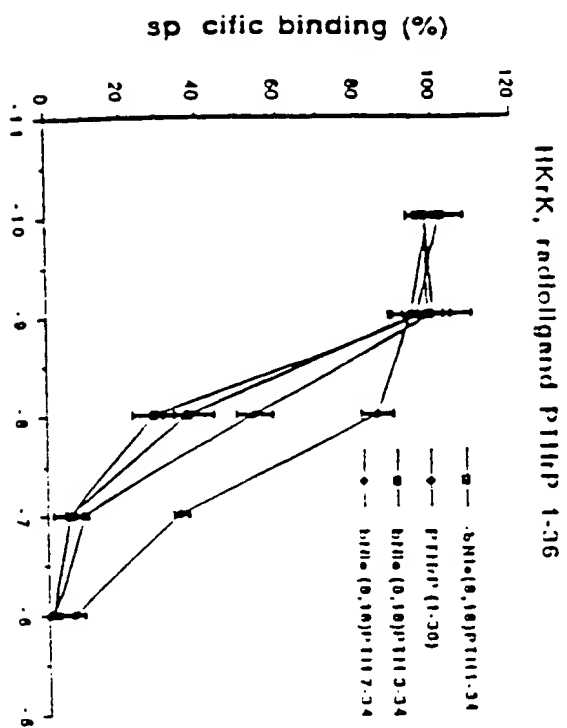
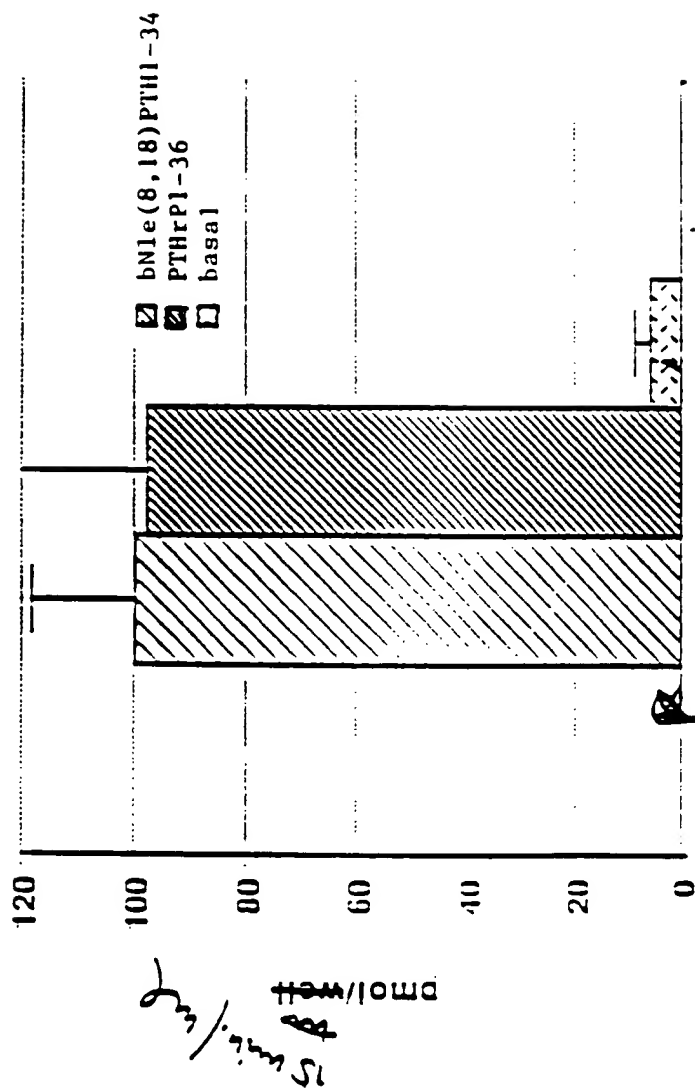


FIG. 16





00100074 112402



00100274-113408



← 185

← 285

A B

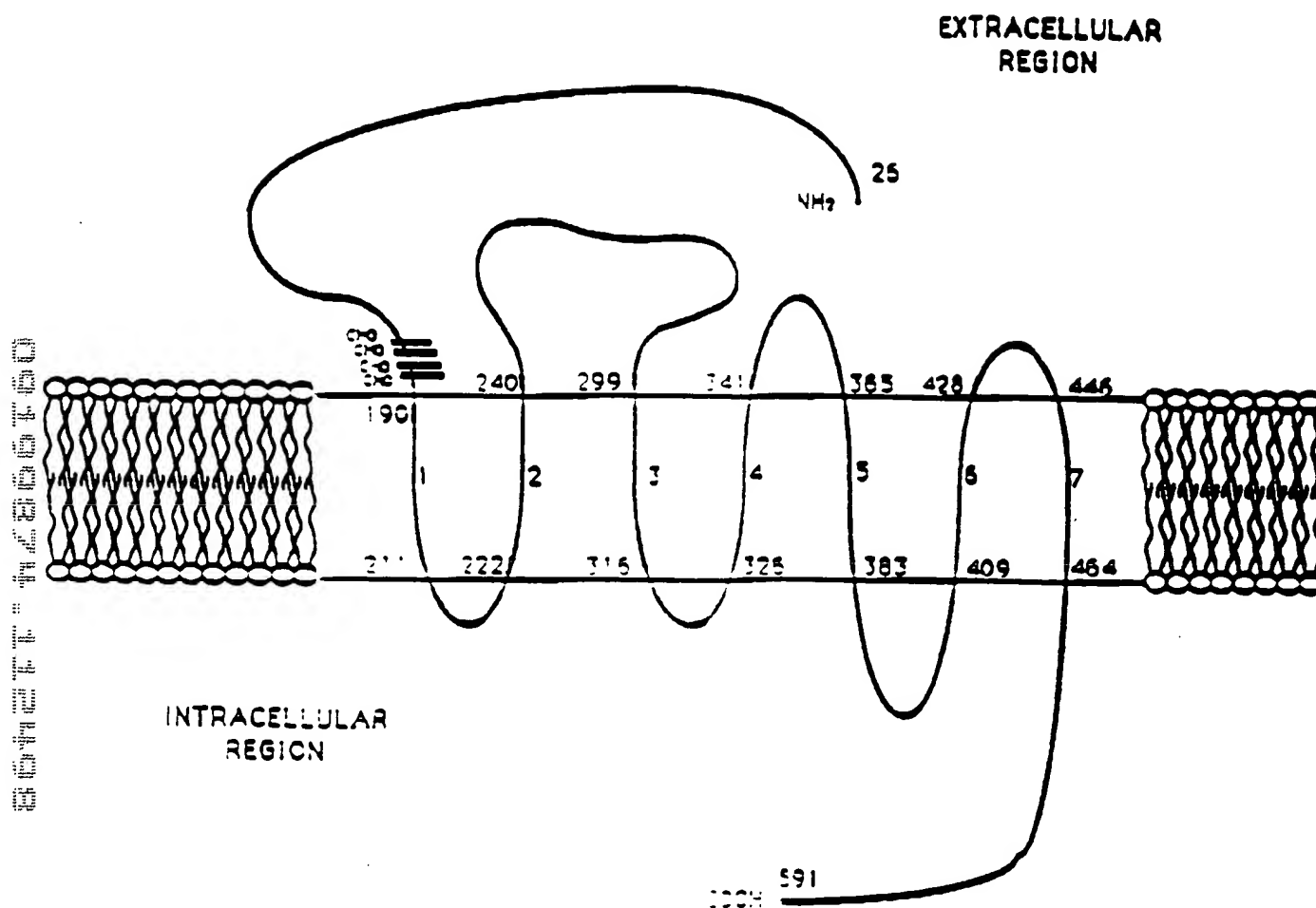
Fig. 9

SECRET - 72850760

(1)



# RAT BONE PTH/PTHrP RECEPTOR



## AMINO ACID SEQUENCE OF 7 PUTATIVE TRANS-MEMBRANE REGIONS

